#5

SEQUENCE LISTING

<110> Houtzager, Erwin
Vijn, Irma Maria Caecilia
Sijmons, Peter Christiaan

<120> A Structure for Presenting Desired Peptide Sequences

<130> 2183-5208US

<140> US 10/016,516
<141> 2001-12-10

<160> 17

<170> PatentIn version 3.1

<210> 1
<211> 291
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' end of exemplary maximal primary scaffold.

<220>
<221> misc_feature
<222> (79)..(93)
<223> The nucleotide at each of positions 79-93 may be any nucleotide.

<220>
<221> misc_feature
<222> (157)..(159)
<223> The nucleotide at each of positions 157-159 may be any nucleotide.

<220>
<221> misc_feature
<222> (214)..(222)
<223> The nucleotide at each of positions 214-222 may be any nucleotide.

<400> 1
aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac gat ctt   54

Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp Asp Leu
1   5   10   15

aag ctc acg tgc cgt gct gaa ggt nnn nnn nnn nnn nnn tac tgc atg ggt tgg   108

Lys Leu Thr Cys Arg Ala Glu Gly Xaa Xaa Xaa Xaa Xaa Tyr Cys Met Gly Trp
        20   25   30   35

ttc cgt cag gcg ccg aac gac gac agt act aac gtg gcc acg atc tta nnn ggg   162

Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val Ala Thr Ile Leu Xaa Gly
            40   45   50

agc acg tac tac ggt gac tcc gtc aaa gag cgc ttc gat atc cgt cgc gac nnn   216

Ser Thr Tyr Tyr Gly Asp Ser Val Lys Glu Arg Phe Asp Ile Arg Arg Asp Xaa
55   60   65   70

nnn nnn aac acc gtt acc tta tcg atg gac gat ctg caa ccg gaa gac tct gca   270

Xaa Xaa Asn Thr Val Thr Leu Ser Met Asp Asp Leu Gln Pro Glu Asp Ser Ala
        75   80   85   90

gaa tac aat tgt gca ggt tct   291

Glu Tyr Asn Cys Ala Gly Ser
                95

<210> 2
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' end of exemplary maximal primary scaffold.

<400> 2
tac cac tac cgt ggt cag ggt acc gac gtt acc gtc tcg tcg   42

Tyr His Tyr Arg Gly Gln Gly Thr Asp Val Thr Val Ser Ser
1   5   10

<210> 3
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Scaffold with V$_{HH}$ 1MEL CDR regions.

<400> 3
aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac gat ctt   54

Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp Asp Leu
1   5   10   15

aag ctc acg tgc cgt gct gaa ggt tac acc att ggc ccg tac tgc atg ggt tgg   108

Lys Leu Thr Cys Arg Ala Glu Gly Tyr Thr Ile Gly Pro Tyr Cys Met Gly Trp
    20   25   30   35

ttc cgt cag gcg ccg aac gac gac agt act aac gtg gcc acg atc aac atg ggt   162

Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val Ala Thr Ile Asn Met Gly
            40   45   50

ggc ggt att acg tac tac ggt gac tcc gtc aaa gag cgc ttc gat atc cgt cgc   216

Gly Gly Ile Thr Tyr Tyr Gly Asp Ser Val Lys Glu Arg Phe Asp Ile Arg Arg
55   60   65   70

gac aac gcg tcc aac acc gtt acc tta tcg atg gac gat ctg caa ccg gaa gac   270

Asp Asn Ala Ser Asn Thr Val Thr Leu Ser Met Asp Asp Leu Gln Pro Glu Asp
        75   80   85   90

tct gca gaa tac aat tgt gca ggt gat tct acc att tac gcg agc tat tat gaa   324

Ser Ala Glu Tyr Asn Cys Ala Gly Asp Ser Thr Ile Tyr Ala Ser Tyr Tyr Glu
                95   100   105

tgt ggt cat ggc ctg agt acc ggc ggt tac ggc tac gat agc cac tac cgt ggt   378

Cys Gly His Gly Leu Ser Thr Gly Gly Tyr Gly Tyr Asp Ser His Tyr Arg Gly
    110   115   120   125

cag ggt acc gac gtt acc gtc tcg tcg   405

Gln Gly Thr Asp Val Thr Val Ser Ser
            130   135

<210> 4
<211> 422
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Scaffold with V$_{HH}$ 1BZQ CDR regions.

<400> 4
aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac gat ctt   54

Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp Asp Leu
1   5   10   15

aag ctc acg tgc cgt gct agc ggt tac gcc tac acg tat atc tac atg ggt tgg   108

Lys Leu Thr Cys Arg Ala Ser Gly Tyr Ala Tyr Thr Tyr Ile Tyr Met Gly Trp
    20   25   30   35

ttc cgt cag gcg ccg aac gac gac agt act aac gtg gcc acc atc gac tcg ggt   162

Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val Ala Thr Ile Asp Ser Gly
            40   45   50

ggc ggc ggt acc ctg tac ggt gac tcc gtc aaa gag cgc ttc gat atc cgt cgc   216

Gly Gly Gly Thr Leu Tyr Gly Asp Ser Val Lys Glu Arg Phe Asp Ile Arg Arg
55   60   65   70

gac aaa ggc tcc aac acc gtt acc tta tcg atg gac gat ctg caa ccg gaa gac   270

Asp Lys Gly Ser Asn Thr Val Thr Leu Ser Met Asp Asp Leu Gln Pro Glu Asp
            75   80   85   90

tct gca gaa tac aat tgt gca gcg ggt ggc tac gaa ctg cgc gac cgc acc tac   324

Ser Ala Glu Tyr Asn Cys Ala Ala Gly Gly Tyr Glu Leu Arg Asp Arg Thr Tyr
                95   100   105

ggt cag cgt ggt cag ggt acc gac gtt acc gtc tcg tcg   383

Gly Gln Arg Gly Gln Gly Thr Asp Val Thr Val Ser Ser
    110   115   120

<210> 5
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Scaffold with V_{HH} 1HCV CDR regions.

<400> 5
aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac gat ctt   54

Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp Asp Leu
1   5   10   15

aag ctc acg tgc cgt gct gaa ggt cgt acg ggt tcg acc tac gat atg ggt tgg   108

Lys Leu Thr Cys Arg Ala Glu Gly Arg Thr Gly Ser Thr Tyr Asp Met Gly Trp
    20   25   30   35

ttc cgt cag gcg ccg aac gac gac agt act aac gtg gcc acg atc aac tgg gat   162

Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val Ala Thr Ile Asn Trp Asp
        40   45   50

agc gcc cgt acg tac tac ggt gac tcc gtc aaa gag cgc ttc gat atc cgt cgc   216

Ser Ala Arg Thr Tyr Tyr Gly Asp Ser Val Lys Glu Arg Phe Asp Ile Arg Arg
55   60   65   70

gac aat gcc tcc aac acc gtt acc tta tcg atg gac gat ctg caa ccg gaa gac   270

Asp Asn Ala Ser Asn Thr Val Thr Leu Ser Met Asp Asp Leu Gln Pro Glu Asp
    75   80   85   90

tct gca gaa tac aat tgt gca ggt ggt gaa ggc ggc acc tgg gat agc cgt ggt   324

Ser Ala Glu Tyr Asn Cys Ala Gly Gly Glu Gly Gly Thr Trp Asp Ser Arg Gly
        95   100   105

cag ggt acc gac gtt acc gtc tcg tcg

Gln Gly Thr Asp Val Thr Val Ser Ser
    110   115

<210> 6
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: T7 primer for amplification of Multiple Cloning
      Sites (MCS) of vector pBluescript KS+.

<400> 6
aatacgactc actatag   17

<210> 7
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: T3 primer for amplification of Multiple Cloning
      Sites (MCS) of vector pBluescript KS+.

<400> 7
attaaccctc actaaag   17   .

<210> 8
<211> 144
<212> PRT
<213> IF2X - Single Domain Camelid Antibody Cab-Ca05

<220>
<221> misc_feature
<222> (7)
<223> The 'Xaa' indicator at position 7 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (10)..(11)
<223> The 'Xaa' indicators at positions 10-11 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (13)
<223> The 'Xaa' indicator at position 13 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (33)..(37)
<223> The 'Xaa' indicators at positions 33-37 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (49)
<223> The 'Xaa' indicator at position 49 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (54)..(55)
<223> The 'Xaa' indicators at positions 54-55 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (65)..(66)
<223> The 'Xaa' indicators at positions 65-66 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (68)..(69)
<223> The 'Xaa' indicators at positions 68-69 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (101)
<223> The 'Xaa' indicator at position 101 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (103)
<223> The 'Xaa' indicator at position 103 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (140)
<223> The 'Xaa' indicator at position 140 indicates the absence of an amino acid residue.

<400> 8

Gln Val Gln Leu Val Glu Xaa Ser Gly Xaa Xaa Gly Xaa Gly Ser Val Gln Ala
1   5   10   15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Xaa Xaa Xaa Xaa
        20   25   30   35

Xaa Val Ser Thr Tyr Cys Met Gly Trp Phe Arg Gln Xaa Ala Pro Gly Lys Xaa
                40   45   50

Xaa Glu Arg Glu Gly Val Ala Thr Ile Leu Xaa Xaa Gly Xaa Xaa Gly Ser Thr
55   60   65   70

Tyr Tyr Gly Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Gln Asp Asn Ala Lys
            75   80   85   90

Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Xaa Lys Xaa Pro Glu Asp Thr Ala
                95   100   105

Ile Tyr Tyr Cys Ala Gly Ser Thr Val Ala Ser Thr Gly Trp Cys Ser Arg Leu
    110   115   120   125

Arg Pro Tyr Asp Tyr His Tyr Arg Gly Gln Gly Thr Gln Xaa Val Thr Val Ser
            130   135   140

<210> 9
<211> 144
<212> PRT
<213> 1QD0 - Camelid Heavy Chain Variable Domain

<220>
<221> misc_feature
<222> (7)
<223> The 'Xaa' indicator at position 7 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (10)..(11)
<223> The 'Xaa' indicators at positions 10-11 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (13)
<223> The 'Xaa' indicator at position 13 indicates the absence of an amino acid residue.

42

<220>
<221> misc_feature
<222> (33)..(34)
<223> The 'Xaa' indicators at positions 33-34 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (49)
<223> The 'Xaa' indicator at position 49 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (54)..(55)
<223> The 'Xaa' indicators at positions 54-55 indicate the absence of amino acid residues

<220>
<221> misc_feature
<222> (68)..(69)
<223> The 'Xaa' indicators at positions 68-69 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (101)
<223> The 'Xaa' indicator at position 101 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (103)
<223> The 'Xaa' indicator at position 103 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (124)..(126)
<223> The 'Xaa' indicators at positions 124-126 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (140)
<223> The 'Xaa' indicator at position 140 indicates the absence of an amino acid residue.

<400> 9
Gln Val Gln Leu Gln Glu Xaa Ser Gly Xaa Xaa Gly Xaa Gly Leu Val Gln Ala
1   5   10   15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Xaa Xaa Ala Ser
     20   25   30   35

Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Xaa Val Pro Gly Lys Xaa
     40   45   50

Xaa Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Xaa Xaa Lys Glu Thr
55   60   65   70

Trp Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
     75   80   85   90

Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Xaa Lys Xaa Gly Glu Asp Thr Ala
           95   100   105

Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Ala Asp Ile Ser Xaa Xaa Xaa
    110   115   120   125

Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Xaa Val Thr Val Ser
      130   135   140

<210> 10
<211> 144
<212> PRT
<213> 8FAB - Heavy Chain from Human Igg1

<220>
<221> misc_feature
<222> (7)
<223> The 'Xaa' indicator at position 7 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (10)..(11)
<223> The 'Xaa' indicators at positions 10-11 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (13)
<223> The 'Xaa' indicator at position 13 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (33)..(37)

<223> The 'Xaa' indicators at positions 33-37 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (49)
<223> The 'Xaa' indicator at position 49 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (54)..(55)
<223> The 'Xaa' indicators at positions 54-55 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (65)..(66)
<223> The 'Xaa' indicators at positions 65-66 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (101)
<223> The 'Xaa' indicator at position 101 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (103)
<223> The 'Xaa' indicator at position 103 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (121)..(127)
<223> The 'Xaa' indicators at positions 121-127 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (140)
<223> The 'Xaa' indicator at position 140 indicates the absence of an amino acid residue.

<400> 10
Ala Val Lys Leu Val Gln Xaa Ala Gly Xaa Xaa Gly Xaa Gly Val Val Gln Pro
1   5   10   15

Gly Arg Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Xaa Xaa Xaa Xaa
    20   25   30   35

45

Xaa Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Xaa Ala Pro Gly Lys Xaa
40   45   50

Xaa Gly Leu Glu Trp Val Ala Val Ile Trp Xaa Xaa Tyr Asn Gly Ser Arg Thr
55   60   65   70

Tyr Tyr Gly Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
75   80   85   90

Arg Thr Leu Tyr Met Gln Met Asn Ser Leu Xaa Arg Xaa Thr Glu Asp Thr Alal
95   100   105

Val Tyr Tyr Cys Ala Arg Asp Pro Asp Ile Leu Thr Xaa Xaa Xaa Xaa Xaa Xaa
110   115   120   125

Xaa Ala Phe Ser Phe Asp Tyr Trp Gly Gln Gly Val Leu Xaa Val Thr Val Ser
130   135   140

<210> 11
<211> 144
<212> PRT
<213> 1VSC - Human Vcam-1

<220>
<221> misc_feature
<222> (1)
<223> The 'Xaa' indicator at position 1 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (7)
<223> The 'Xaa' indicator at position 7 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (13)
<223> The 'Xaa' indicator at position 13 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (33)..(39)
<223> The 'Xaa' indicators at positions 33-39 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (49)
<223> The 'Xaa' indicator at position 49 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (52)..(77)
<223> The 'Xaa' indicators at positions 52-77 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (89)..(90)
<223> The 'Xaa' indicators at positions 89-90 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (101)
<223> The 'Xaa' indicator at position 101 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (103)
<223> The 'Xaa' indicator at position 103 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (118)..(129)
<223> The 'Xaa' indicators at positions 118-129 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (136)
<223> The 'Xaa' indicator at position 136 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (140)
<223> The 'Xaa' indicator at position 140 indicates the absence of an amino acid residue.

<400> 11
Xaa Phe Lys Ile Glu Thr Xaa Thr Pro Glu Ser Arg Xaa Tyr Leu Ala Gln Ile
1   5   10   15

Gly Asp Ser Val Ser Leu Thr Cys Ser Thr Thr Gly Cys Glu Xaa Xaa Xaa Xaa
   20   25   30   35

Xaa Xaa Xaa Ser Pro Phe Phe Ser Trp Arg Thr Gln Xaa Ile Asp Xaa Xaa Xaa
        40   45   50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
55   60   65   70

Xaa Xaa Xaa Xaa Xaa Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Xaa Xaa
     75   80   85   90

Thr Thr Ser Thr Leu Thr Met Asn Pro Val Xaa Ser Xaa Phe Gly Asn Glu His
           95   100   105

Ser Tyr Leu Cys Thr Ala Thr Cys Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
   110   115   120   125

Xaa Xaa Xaa Ser Arg Lys Leu Glu Lys Xaa Gly Ile Gln Xaa Val Glu Ile Tyr
        130   135   140

<210> 12
<211> 144
<212> PRT
<213> 1NS3 - Structure of Hcv Protease (Bk Strain) from Hepatitis C-virus

<220>
<221> misc_feature
<222> (7)
<223> The 'Xaa' indicator at position 7 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (10)..(11)
<223> The 'Xaa' indicators at positions 10-11 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (13)..(20)
<223> The 'Xaa' indicators at positions 13-20 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (31)..(39)

<223> The 'Xaa' indicators at positions 31-39 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (49)
<223> The 'Xaa' indicator at position 49 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (51)..(57)
<223> The 'Xaa' indicators at positions 51-57 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (63)..(83)
<223> The 'Xaa' indicators at positions 63-83 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (101)
<223> The 'Xaa' indicator at position 101 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (103)
<223> The 'Xaa' indicator at position 103 indicates the absence of an amino acid residue

<220>
<221> misc_feature
<222> (140)
<223> The 'Xaa' indicator at position 140 indicates the absence of an amino acid residue.

<400> 12
Thr Gln Ser Phe Leu Ala Xaa Thr Cys Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Asn Gly Val Cys Trp Thr Val Tyr His Gly Xaa Xaa Xaa Xaa Xaa Xaa
    20   25   30   35

Xaa Xaa Xaa Ala Gly Ser Lys Thr Leu Ala Gly Pro Xaa Lys Xaa Xaa Xaa Xaa
        40   45   50

Xaa Xaa Xaa Gly Pro Ile Thr Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
55   60   65   70

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Met Tyr Thr Trp Val Asp Gln
       75   80   85   90

Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Xaa Ala Xaa Arg Ser Leu Thr Pro
        95   100   105

Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile
   110   115   120   125

Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Xaa Ser Pro Arg Pro
       130   135   140

<210> 13
<211> 144
<212> PRT
<213> 1F97 - Soluble Part of the Junction Adhesion Molecule from a Mouse

<220>
<221> misc_feature
<222> (7)
<223> The 'Xaa' indicator at position 7 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (11)
<223> The 'Xaa' indicator at position 11 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (13)
<223> The 'Xaa' indicator at position 13 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (33)..(39)
<223> The 'Xaa' indicators at positions 33-39 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (49)
<223> The 'Xaa' indicator at position 49 indicates the absence of an amino acid residue

<220>
<221> misc_feature

<222> (51)
<223> The 'Xaa' indicator at position 51 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (54)..(55)
<223> The 'Xaa' indicators at positions 54-55 indicate the absence of amino acid residues

<220>
<221> misc_feature
<222> (65)..(72)
<223> The 'Xaa' indicators at positions 65-72 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (87)..(92)
<223> The 'Xaa' indicators at positions 87-92 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (101)
<223> The 'Xaa' indicator at position 101 indicates the absence of an amino acid residue

<220>
<221> misc_feature
<222> (103)
<223> The `Xaa` indicator at position 103 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (121)..(131)
<223> The 'Xaa' indicators at positions 121-131 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (140)
<223> The 'Xaa' indicator at position 140 indicates the absence of an amino acid residue.

<400> 13
Lys Gly Ser Val Tyr Thr Xaa Ala Gln Ser Xaa Asp Xaa Val Gln Val Pro Glu
1   5   10   15

Asn Glu Ser Ile Lys Leu Thr Cys Thr Tyr Ser Gly Phe Ser Xaa Xaa Xaa Xaa
    20   25   30   35

Xaa Xaa Xaa Ser Pro Arg Val Glu Trp Lys Phe Val Xaa Gln Xaa Gly Ser Xaa
      40   45   50

Xaa Thr Thr Ala Leu Val Cys Tyr Asn Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
55   60   65   70

Gln Ile Thr Ala Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Xaa Xaa Xaa Xaa
      75   80   85   90

Xaa Xaa Ser Gly Ile Thr Phe Ser Ser Val Xaa Thr Xaa Arg Lys Asp Asn Gly
          95   100   105

Glu Tyr Thr Cys Met Val Ser Asx Glu Gly Gly Gln Xaa Xaa Xaa Xaa Xaa Xaa
    110   115   120   125

Xaa Xaa Xaa Xaa Xaa Asn Tyr Gly Glu Val Ser Ile His Xaa Leu Thr Val Leu
      130   135   140

<210> 14
<211> 144
<212> PRT
<213> IFNF - Fragment of Human Fibronectin Encompassing Type-III Repeats 7 through 10

<220>
<221> misc_feature
<222> (7)
<223> The 'Xaa' indicator at position 7 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (10)..(11)
<223> The 'Xaa' indicators at positions 10-11 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (18)..(19)
<223> The 'Xaa' indicators at positions 18-19 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (32)..(37)
<223> The 'Xaa' indicators at positions 32-37 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (54)..(55)
<223> The 'Xaa' indicators at positions 54-55 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (65)..(89)
<223> The 'Xaa' indicators at positions 65-89 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (101)
<223> The 'Xaa' indicator at position 101 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (103)
<223> The 'Xaa' indicator at position 103 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (120)..(130)
<223> The 'Xaa' indicators at positions 118-128 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (136)
<223> The 'Xaa' indicator at position 136 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (140)
<223> The 'Xaa' indicator at position 140 indicates the absence of an amino acid residue.

<400> 14
Val Pro Pro Pro Thr Asp Xaa Leu Arg Xaa Xaa Thr Thr Asn Ile Gly Pro Xaa
1   5   10   15

Xaa Asp Thr His Arg Val Thr Trp Ala Pro Pro Pro Ser Xaa Xaa Xaa Xaa Xaa
    20   25   30   35

Xaa Ile Asp Leu Thr Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Met Glu Xaa
        40   45   50

53

Xaa Glu Asp Val Ala Glu Leu Ser Ile Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
55   60   65   70

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
        75   80   85   90

Ser Asp Asn Ala Val Val Leu Thr Asn Leu Xaa Leu Xaa Pro Gly Thr Glu Tyr
                95   100   105

Val Val Ser Val Ser Ser Val Tyr Glu Gln His Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        110   115   120   125

Xaa Xaa Xaa Xaa Glu Ser Thr Pro Leu Xaa Arg Gly Arg Xaa Gln Lys Thr Gly
            130   135   140

<210> 15
<211> 144
<212> PRT
<213> 1CFB - Drosophila neuroglian

<220>
<221> misc_feature
<222> (10)..(11)
<223> The 'Xaa' indicators at positions 10-11 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (13)
<223> The 'Xaa' indicator at position 13 indicates the absence of an amino acid residue.

<220>
<221> misc_feature

<222> (18)..(20)
<223> The 'Xaa' indicators at positions 18-20 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (33)..(36)
<223> The 'Xaa' indicators at positions 33-36 indicate the absence of amino acid residues

<220>
<221> misc_feature
<222> (49)

<223> The 'Xaa' indicator at position 49 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (65)..(88)
<223> The 'Xaa' indicators at positions 65-88 indicate the absence of amino acid residues

<220>
<221> misc_feature
<222> (101)..(103)
<223> The 'Xaa' indicators at positions 101-103 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (118)..(128)
<223> The 'Xaa' indicators at positions 118-128 indicate the absence of amino acid residues.

<400> 15
Pro Asn Ala Pro Lys Leu Thr Gly Ile Xaa Xaa Thr Xaa Cys Gln Ala Asp Xaa
1   5   10   15

Xaa Xaa Lys Ala Glu Ile His Trp Glu Gln Gln Gly Asp Asn Xaa Xaa Xaa Xaa
    20   25   30   35

Arg Ser Pro Ile Leu His Tyr Thr Ile Gln Phe Asn Xaa Thr Ser Phe Thr Pro
            40   45   50

Ala Ser Trp Asp Ala Ala Tyr Glu Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
55   60   65   70

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Asn
        75   80   85   90
Thr Asp Ser Ser Phe Val Val Gln Met Ser Xaa Xaa Xaa Pro Trp Ala Asn Tyr
            95   100   105

Thr Phe Arg Val Ile Ala Phe Asn Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    110   115   120   125

Xaa Xaa Ile Gly Ala Ser Pro Pro Ser Ala His Ser Asp Ser Cys Thr Thr Gln
            130   135   140

<210> 16
<211> 144
<212> PRT

55

<213> 1IAR - Human Interleukin-4 Receptor Alpha Chain Complex

<220>
<221> misc_feature
<222> (7)
<223> The 'Xaa' indicator at position 7 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (12)..(16)
<223> The 'Xaa' indicators at positions 12-16 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (49)
<223> The 'Xaa' indicator at position 49 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (54)..(55)
<223> The 'Xaa' indicators at positions 54-55 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (65)..(90)
<223> The 'Xaa' indicators at positions 65-90 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (101)
<223> The 'Xaa' indicator at position 101 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (122)..(128)
<223> The 'Xaa' indicators at positions 122-128 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (141)
<223> The 'Xaa' indicator at position 141 indicates the absence of an amino acid residue.

<400> 16
Arg Ala Pro Gly Asn Leu Xaa Thr Val Asn Thr Xaa Xaa Xaa Xaa Xaa Asn Val
1   5   10   15

Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu
    20   25   30   35

Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Ser Glu Xaa Asn Asp Pro Ala Xaa
            40   45   50

Xaa Asp Glu Arg Ile Tyr Asn Val Thr Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
55   60   65   70

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        75   80   85   90

Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Xaa Thr Leu Lys Ser Gly Ile Ser
                95   100   105

Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Ala Tyr Asn Xaa Xaa Xaa Xaa Xaa
    110   115   120   125

Xaa Xaa Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp Xaa His Asn Ser
        130   135   140

<210> 17
<211> 144
<212> PRT
<213> 1F4H - E. Coli (Lacz) Beta-Galactosidase (Orthorhombic)

<220>
<221> misc_feature
<222> (7)
<223> The 'Xaa' indicator at position 7 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (10)..(23)
<223> The 'Xaa' indicators at positions 10-23 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (33)
<223> The 'Xaa' indicator at position 33 indicates the absence of an amino acid residue.

57

<220>
<221> misc_feature
<222> (49)
<223> The 'Xaa' indicator at position 49 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (53)..(55)
<223> The 'Xaa' indicators at positions 53-55 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (65)..(66)
<223> The 'Xaa' indicators at positions 65-66 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (69)..(70)
<223> The 'Xaa' indicators at positions 69-70 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (72)..(85)
<223> The 'Xaa' indicators at positions 72-85 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (103)
<223> The 'Xaa' indicator at position 103 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (123)..(125)
<223> The 'Xaa' indicators at positions 123-125 indicate the absence of amino acid residues.

<220>
<221> misc_feature
<222> (136)
<223> The 'Xaa' indicator at position 136 indicates the absence of an amino acid residue.

<220>
<221> misc_feature
<222> (140)
<223> The 'Xaa' indicator at position 140 indicates the absence of an amino acid residue.

<400> 17
Phe Phe Gln Phe Arg Leu Xaa Ser Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Gln Thr Ile Glu Val Thr Ser Glu Tyr Xaa Leu Phe Arg
    20   25   30   35

His Ser Asp Asn Glu Leu Leu His Trp Met Val Ala Xaa Leu Asp Gly Xaa Xaa
            40   45   50

Xaa Lys Pro Leu Ala Ser Gly Glu Val Pro Xaa Xaa Leu Asp Xaa Xaa Val Xaa
55   60   65   70

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Pro Gln Gly Lys
        75   80   85   90

Gln Leu Ile Glu Leu Pro Glu Leu Pro Gly Pro Glu Xaa Ser Ala Gly Gln Leu
            95   100   105

Trp Leu Thr Val Arg Val Val Gln Pro Asn Ala Thr Ala Trp Xaa Xaa Xaa Ser
    110   115   120   125

Glu Ala Gly His Ile Ser Ala Trp Gln Xaa Gln Trp Arg Xaa Leu Ala Glu Asn
        130   135   140

<210> 18
<211> 363
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Artificial Sequence: Exemplary primary scaffold used to obtain optimal secondary
      scaffolds.

<220>
<221> misc_feature
<222> (73)..(99)
<223> The nucleotide at positions 73-99 may be any nucleotide.

<220>
<221> misc_feature
<222> (157)..(177)
<223> The nucleotide at positions 157-177 may be any nucleotide.

<220>
<221> misc_feature
<222> (292)..(333)
<223> The nucleotide at positions 292-333 may be any nucleotide

<400> 18
aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa aac gat gac gat ctt   54

Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp Asp Leu
1   5   10   15

aag ctc acg tgc cgt gct nnn nnn nnn nnn nnn nnn nnn nnn nnn atg ggt tgg 108

Lys Leu Thr Cys Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Met Gly Trp
   20   25   30   35

ttc cgt cag gcg ccg aac gac gac agt act aac gtg gcc acc atc gac nnn nnn 162

Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val Ala Thr Ile Asp Xaa Xaa
      40   45   50

nnn nnn nnn nnn nnn tac ggt gac tcc gtc aaa gag cgc ttc gat atc cgt cgc 216

Xaa Xaa Xaa Xaa Xaa Tyr Gly Asp Ser Val Lys Glu Arg Phe Asp Ile Arg Arg
55   60   65   70

gac aaa ggc tcc aac acc gtt acc tta tcg atg gac gat ctg caa ccg gaa gac 270

Asp Lys Gly Ser Asn Thr Val Thr Leu Ser Met Asp Asp Leu Gln Pro Glu Asp
   75   80   85   90

tct gca gaa tac aat tgt gca nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn 324

Ser Ala Glu Tyr Asn Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      95   100   105

nnn nnn nnn ggt cag ggt acc gac gtt acc gtc tcg tcg   363

Xaa Xaa Xaa Gly Gln Gly Thr Asp Val Thr Val Ser Ser
   110   115   120